

Bayesian approach to modeling HIV viral rebound

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Abstract

Viral dynamics is a relatively new field of study that relies on mathematical models to describe the temporal evolution of virus levels in the blood plasma, the so-called viral load. Our scientific aim is to find a flexible, yet parsimonious mechanistic model based on ordinary differential equations (ODE) for the so-called rebounders, a special subgroup of patients who, after an initial decrease in viral load levels, show a sudden rise in viral load levels during treatment. This rebound is generally caused by the emergence of a drug-resistant virus strain. The data of rebounders analyzed come from pooling three clinical trials on Prezista, a recently developed protease inhibitor. Different aspects of a Bayesian modeling approach will be discussed and implemented in MONOLIX.

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